

SEQUENCE LISTING

<110> Powers, Scott
Yang, Jianxin
Cutler, Gene
Tularik Inc.

<120> Novel G-Protein Coupled Receptors

<130> 018781-004730US

<140> US Not yet assigned

<141> Not yet assigned

<150> US 09/524,730

<151> 2000-03-14

<150> US 09/546,986

<151> 2001-04-11

<160> 23

<170> PatentIn Ver. 2.1

<210> 1

<211> 1035

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (42)..(974)

<223> human breast cancer amplified G-protein coupled
receptor 1 (BCA-GPCR-1)

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Leu Leu Gly Asp Ser
1 5

cct aaa gcc ttc atc ctt ctg ggt gtg tct gac agg ccg tgg ctg gaa 104
Pro Lys Ala Phe Ile Leu Leu Gly Val Ser Asp Arg Pro Trp Leu Glu
10 15 20

ctc cct ctc ttt gtg gtc ctc ctg ctg tcc tat gtg ctg gcc atg ttg 152
Leu Pro Leu Phe Val Val Leu Leu Leu Ser Tyr Val Leu Ala Met Leu
25 30 35

ggg aac gtc gcc atc atc ctg gca tcc cgg gtg gat cct caa ctc cac 200
Gly Asn Val Ala Ile Ile Leu Ala Ser Arg Val Asp Pro Gln Leu His
40 45 50

agc ccc atg tac atc ttc ctc agt cac ctg tcc ttc ctg gac ctc tgc 248
Ser Pro Met Tyr Ile Phe Leu Ser His Leu Ser Phe Leu Asp Leu Cys
55 60 65

tac acc acc acg aca gtc cct cag atg ctg gtc aac atg ggc agt tcc 296
Tyr Thr Thr Thr Thr Val Pro Gln Met Leu Val Asn Met Gly Ser Ser
70 75 80 85

cag aag acc atc agc tat gga ggc tgc act gtg caa tat gca gtc ttc	344
Gln Lys Thr Ile Ser Tyr Gly Gly Cys Thr Val Gln Tyr Ala Val Phe	
90 95 100	
cac tgg ctg gga tgc acg gag tgc atc gtc ctg gcc gcc atg gcc ctg	392
His Trp Leu Gly Cys Thr Glu Cys Ile Val Leu Ala Ala Met Ala Leu	
105 110 115	
gac cgc tac gtg gcc agc tgc aag ccc ctg cac tat gcc gtt ctc atg	440
Asp Arg Tyr Val Ala Ser Cys Lys Pro Leu His Tyr Ala Val Leu Met	
120 125 130	
cac cgt gct ctc tgt cag cag ctc gtg gct ctg gcc tgg ctc agt ggc	488
His Arg Ala Leu Cys Gln Gln Leu Val Ala Leu Ala Trp Leu Ser Gly	
135 140 145	
ttc ggc aac tcc ttc gtg cag gtg gtc ctg acg gtg caa ttg cca ttc	536
Phe Gly Asn Ser Phe Val Gln Val Val Leu Thr Val Gln Leu Pro Phe	
150 155 160 165	
tgc ggg cgg cag gtg ctg aac aac ttt ttc tgt gag gtg ccg gcc gtg	584
Cys Gly Arg Gln Val Leu Asn Asn Phe Phe Cys Glu Val Pro Ala Val	
170 175 180	
atc aag ctg tgc tgt gct gac acc gct atg aat gac acc ata ctg gct	632
Ile Lys Leu Ser Cys Ala Asp Thr Ala Met Asn Asp Thr Ile Leu Ala	
185 190 195	
gtg ctg gtg gcc ttc ttc gtg ttg gtg ccc ctg gct ctc atc ctt ctc	680
Val Leu Val Ala Phe Phe Val Leu Val Pro Leu Ala Leu Ile Leu Leu	
200 205 210	
tcc tat ggc ttt att gcc cgg gca gtg ctc agg atc cag tcc tcc aag	728
Ser Tyr Gly Phe Ile Ala Arg Ala Val Leu Arg Ile Gln Ser Ser Lys	
215 220 225	
gga cga cac aag gcc ttt ggg acg tgt tcc tcc cac ctg atg atc gtc	776
Gly Arg His Lys Ala Phe Gly Thr Cys Ser Ser His Leu Met Ile Val	
230 235 240 245	
tcc ctc ttc tac cta cct gcg att tac atg tat ctg cag ccc cct tcc	824
Ser Leu Phe Tyr Leu Pro Ala Ile Tyr Met Tyr Leu Gln Pro Pro Ser	
250 255 260	
agc tac tcc caa gag cag ggc aaa ttt att tct ctc ttc tat tcc ata	872
Ser Tyr Ser Gln Glu Gln Gly Lys Phe Ile Ser Leu Phe Tyr Ser Ile	
265 270 275	
atc acc ccc act ctc aat ccc ttc acc tac acc ctg aga aat aaa gat	920
Ile Thr Pro Thr Leu Asn Pro Phe Thr Tyr Thr Leu Arg Asn Lys Asp	
280 285 290	
atg aag ggg gct ctg agg aga ctt ctg gcc agg atc tgg agg ctc tgt	968
Met Lys Gly Ala Leu Arg Arg Leu Leu Ala Arg Ile Trp Arg Leu Cys	
295 300 305	
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Gly	
310	
ctattgtgca c	1035

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 <213> Homo sapiens

<220>
 <223> human breast cancer amplified G-protein coupled
 receptor 1 (BCA-GPCR-1)

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 Arg Pro Trp Leu Glu Leu Pro Leu Phe Val Val Leu Leu Ser Tyr
 20 25 30
 Val Leu Ala Met Leu Gly Asn Val Ala Ile Ile Leu Ala Ser Arg Val
 35 40 45
 Asp Pro Gln Leu His Ser Pro Met Tyr Ile Phe Leu Ser His Leu Ser
 50 55 60
 Phe Leu Asp Leu Cys Tyr Thr Thr Thr Thr Val Pro Gln Met Leu Val
 65 70 75 80
 Asn Met Gly Ser Ser Gln Lys Thr Ile Ser Tyr Gly Gly Cys Thr Val
 85 90 95
 Gln Tyr Ala Val Phe His Trp Leu Gly Cys Thr Glu Cys Ile Val Leu
 100 105 110
 Ala Ala Met Ala Leu Asp Arg Tyr Val Ala Ser Cys Lys Pro Leu His
 115 120 125
 Tyr Ala Val Leu Met His Arg Ala Leu Cys Gln Gln Leu Val Ala Leu
 130 135 140
 Ala Trp Leu Ser Gly Phe Gly Asn Ser Phe Val Gln Val Val Leu Thr
 145 150 155 160
 Val Gln Leu Pro Phe Cys Gly Arg Gln Val Leu Asn Asn Phe Phe Cys
 165 170 175
 Glu Val Pro Ala Val Ile Lys Leu Ser Cys Ala Asp Thr Ala Met Asn
 180 185 190
 Asp Thr Ile Leu Ala Val Leu Val Ala Phe Phe Val Leu Val Pro Leu
 195 200 205
 Ala Leu Ile Leu Leu Ser Tyr Gly Phe Ile Ala Arg Ala Val Leu Arg
 210 215 220
 Ile Gln Ser Ser Lys Gly Arg His Lys Ala Phe Gly Thr Cys Ser Ser
 225 230 235 240
 His Leu Met Ile Val Ser Leu Phe Tyr Leu Pro Ala Ile Tyr Met Tyr
 245 250 255
 Leu Gln Pro Pro Ser Ser Tyr Ser Gln Glu Gln Gly Lys Phe Ile Ser
 260 265 270
 Leu Phe Tyr Ser Ile Ile Thr Pro Thr Leu Asn Pro Phe Thr Tyr Thr
 275 280 285
 Leu Arg Asn Lys Asp Met Lys Gly Ala Leu Arg Arg Leu Leu Ala Arg
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 Ile Trp Arg Leu Cys Gly
 305 310

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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (118)..(1113)
 <223> human breast cancer amplified G-protein coupled
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 ctgcattgtc ccccttatct aattctttgg ttgtttctct gtaatatgctg gtggatt 117
 atg gga aag gac aat gcc agt tac cta cag gca ttc atc ctg gtg ggc 165
 Met Gly Lys Asp Asn Ala Ser Tyr Leu Gln Ala Phe Ile Leu Val Gly
 1 5 10 15
 tct tct gat cgg cct gga ctg gag aaa att ctc ttt gct gtt atc ttg 213
 Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu
 20 25 30
 atc ttc tgc atc ctg acc ctg gtg ggc aac act gcc atc atc ctc ttg 261
 Ile Phe Cys Ile Leu Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Leu
 35 40 45
 ctg gtc atg gat gtc agg ctc cac aca ccc atg tac ttc ttt ctt ggg 309
 Leu Val Met Asp Val Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
 50 55 60
 aat ctg tct ttc tta gat ctc tgc ttt aca gca agc att gcc cct cag 357
 Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
 65 70 75 80
 ctg ctg tgg aac ctg ggg ggt cca gag aag acc atc acc tac cac ggc 405
 Leu Leu Trp Asn Asn Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
 85 90 95
 tgt gtg gcc caa ctc tac atc tac atg atg ctg ggc tcc acc gag tgc 453
 Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
 100 105 110
 gtc ctc ctg gtt gtc atg tcc cat gac cgc tat gtg gcc gtc tgc cgg 501
 Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
 115 120 125
 tcc ctg cac tac atg gca gtc atg cgc cca cat ctc tgc ctg cag ctg 549
 Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
 130 135 140
 gtg act gtg gcc tgg tgc tgt ggc ttc cta aac tcc ttc atc atg tgt 597
 Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
 145 150 155 160
 cct cag acg atg cag ctc tcc cgg tgt gga cgt cgc agg gtg gac cac 645
 Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
 165 170 175
 ttc ctg tgt gag atg cct gct ctt att gcc atg tct tgt gag gaa acc 693
 Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
 180 185 190

atg ctg gta gaa gog att cac ctt tgc cct ggg ggt ggc tct cct cct 741
 Met Leu Val Glu Ala Ile His Leu Cys Pro Gly Gly Ser Pro Pro
 195 200 205

ggt gcc gct ctc cct cat cct cat ctc tat ggc gtg att gca gcc gcg 789
 Gly Ala Ala Leu Pro His Pro His Leu Tyr Gly Val Ile Ala Ala Ala
 210 215 220

gtg ctg agg atg aag tca gca gca ggg cga aag aaa gcc ttc cac acc 837
 Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
 225 230 235 240

tgc tct tct cac ctc aca gtg gtc tct ctc ttc tac gga acc atc atc 885
 Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Thr Ile Ile
 245 250 255

tac gtg tac ctg aag ccg gcc aac agc tac tcc caa gat cag ggg aag 933
 Tyr Val Tyr Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp Gln Gly Lys
 260 265 270

ttc ctg act ctc ttc tac acc atc gtc att ccc agc atc aac ccc ctc 981
 Phe Leu Thr Leu Phe Tyr Thr Ile Val Ile Pro Ser Ile Asn Pro Leu
 275 280 285

atc tac act ttg agg aac aag gat gtg aag ggg acc atg aag aaa ctt 1029
 Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Thr Met Lys Lys Leu
 290 295 300

ctg ggg tgg gag aaa ggg gct ggg gag cct caa cga ggg gaa cac tct 1077
 Leu Gly Trp Glu Lys Gly Ala Gly Glu Pro Gln Arg Gly Glu His Ser
 305 310 315 320

agt aat gta gac agt ttg ctg gag tta ctc tct tag atgtgtctgt 1123
 Ser Asn Val Asp Ser Leu Leu Glu Leu Leu Ser
 325 330

ggccatgtgg agaactaata ttcaaggagt agagtgaacg cgggtgggaa aatgctttcg 1183

agtttgaccc cgtcctctgc cctctggatg tgaagtgggt tccttctgtt tgaagttgcc 1243

tgcttcagga tatctctgct gtatcttgca ctttcttctgt ctttttgatt tatccacaac 1303

tgctggggac ttacaaaact aattcaatca cccaaaggca ctgggcagtc tgcagattat 1363

gtcatggatg tcaataaaaa attgagacaa catgaaaaaa aaaaaaaa 1411

<210> 4

<211> 331

<212> PRT

<213> Homo sapiens

<220>

<223> human breast cancer amplified G-protein coupled
receptor 2 (BCA-GPCR-2)

<400> 4

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 1 5 10 15
 Ser Ser Asp Arg Pro Gly Leu Glu Lys Ile Leu Phe Ala Val Ile Leu
 20 25 30

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Ile Phe Cys Ile Leu Thr Leu Val Gly Asn Thr Ala Ile Ile Leu Leu
      35          40          45
Leu Val Met Asp Val Arg Leu His Thr Pro Met Tyr Phe Phe Leu Gly
      50          55          60
Asn Leu Ser Phe Leu Asp Leu Cys Phe Thr Ala Ser Ile Ala Pro Gln
      65          70          75          80
Leu Leu Trp Asn Leu Gly Gly Pro Glu Lys Thr Ile Thr Tyr His Gly
      85          90          95
Cys Val Ala Gln Leu Tyr Ile Tyr Met Met Leu Gly Ser Thr Glu Cys
      100          105          110
Val Leu Leu Val Val Met Ser His Asp Arg Tyr Val Ala Val Cys Arg
      115          120          125
Ser Leu His Tyr Met Ala Val Met Arg Pro His Leu Cys Leu Gln Leu
      130          135          140
Val Thr Val Ala Trp Cys Cys Gly Phe Leu Asn Ser Phe Ile Met Cys
      145          150          155          160
Pro Gln Thr Met Gln Leu Ser Arg Cys Gly Arg Arg Arg Val Asp His
      165          170          175
Phe Leu Cys Glu Met Pro Ala Leu Ile Ala Met Ser Cys Glu Glu Thr
      180          185          190
Met Leu Val Glu Ala Ile His Leu Cys Pro Gly Gly Gly Ser Pro Pro
      195          200          205
Gly Ala Ala Leu Pro His Pro His Leu Tyr Gly Val Ile Ala Ala Ala
      210          215          220
Val Leu Arg Met Lys Ser Ala Ala Gly Arg Lys Lys Ala Phe His Thr
      225          230          235          240
Cys Ser Ser His Leu Thr Val Val Ser Leu Phe Tyr Gly Thr Ile Ile
      245          250          255
Tyr Val Tyr Leu Lys Pro Ala Asn Ser Tyr Ser Gln Asp Gln Gly Lys
      260          265          270
Phe Leu Thr Leu Phe Tyr Thr Ile Val Ile Pro Ser Ile Asn Pro Leu
      275          280          285
Ile Tyr Thr Leu Arg Asn Lys Asp Val Lys Gly Thr Met Lys Lys Leu
      290          295          300
Leu Gly Trp Glu Lys Gly Ala Gly Glu Pro Gln Arg Gly Glu His Ser
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Ser Asn Val Asp Ser Leu Leu Glu Leu Leu Ser
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<211> 1351

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (86)..(1108)

<223> human breast cancer amplified G-protein coupled
receptor 3-A (BCA-GPCR-3-A)

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aactgatgta attgtctcat gtctc atg ccc tgt atg ccc tgt gct ctt ccc 112
      Met Pro Cys Met Pro Cys Ala Leu Pro
      1          5

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aca ggt ggc ctt ttg ccc cac ccc cag cat aca atg atg gaa ata gcc 160
Thr Gly Gly Leu Leu Pro His Pro Gln His Thr Met Met Glu Ile Ala
      10          15          20          25

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aat gtg agt tct cca gaa gtc ttt gtc ctc ctg ggc ttc tcc gca cga	208
Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly Phe Ser Ala Arg	
30 35 40	
ccc tca cta gaa act gtc ctc ttc ata gtt gtc ttg agt ttt tac atg	256
Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu Ser Phe Tyr Met	
45 50 55	
gta tcg atc ttg ggc aat ggc atc atc att ctg gtc tcc cat aca gat	304
Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val Ser His Thr Asp	
60 65 70	
gtg cac ctc cac aca cct atg tac ttc ttt ctt gcc aac ctc tcc ttc	352
Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser Phe	
75 80 85	
ctg gac atg agc ttc acc acg agc att gtc cca cag ctc ctg gct aac	400
Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln Leu Leu Ala Asn	
90 95 100 105	
ctc tgg gga cca cag aaa acc ata agc tat gga ggg tgt gtg gtc cag	448
Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly Cys Val Val Gln	
110 115 120	
ttc tat atc tcc cat tgg ctg ggg gca acc gag tgt gtc ctg ctg gcc	496
Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys Val Leu Leu Ala	
125 130 135	
acc atg tcc tat gac cgc tac gct gcc atc tgc agg cca ctc cat tac	544
Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg Pro Leu His Tyr	
140 145 150	
act gtc att atg cat cca cag ott tgc ott ggg cta gct ttg gcc tcc	592
Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu Ala Leu Ala Ser	
155 160 165	
tgg ctg ggg ggt ctg acc acc agc atg gtg ggc tcc acg ctc acc atg	640
Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser Thr Leu Thr Met	
170 175 180 185	
ctc cta cag ctg tgt ggg aac aat tgc atc gac cac ttc ttt tgc gag	688
Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His Phe Phe Cys Glu	
190 195 200	
atg ccc ctc att atg caa ctg gct tgt gtg gat acc agc ctc aat gag	736
Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr Ser Leu Asn Glu	
205 210 215	
atg gag atg tac ctg gcc agc ttt gtc ttt gtt gtc ctg cct ctg ggg	784
Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val Leu Pro Leu Gly	
220 225 230	
ctc atc ctg gtc tct tac ggc cac att gcc cgg gcc gtg ttg aag atc	832
Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala Val Leu Lys Ile	
235 240 245	
agg tca gca gaa ggg cgg aga aag gca ttc aac acc tgt tct tcc cac	880
Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr Cys Ser Ser His	
250 255 260 265	

gtg gct gtg gtg tct ctg ttt tac ggg agc atc atc ttc atg tat ctc 928
Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile Phe Met Tyr Leu
270 275 280

cag cca gcc aag agc acc tcc cat gag cag ggc aag ttc ata gct ctg 976
Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys Phe Ile Ala Leu
285 290 295

ttc tac acc gta gtc act cct gcg ttg aac cca ctt att tac acc ctg 1024
Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu Ile Tyr Thr Leu
300 305 310

agg aac acg gag gtg aag agc gcc ctc cgg cac atg gta tta gag aac 1072
Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met Val Leu Glu Asn
315 320 325

tgc tgt ggc tct gca ggc aag ctg gcg caa att tag agactccagt 1118
Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
330 335 340

gccttctgag aaggaagatc aagtttcatc cgagcaaagt gaccttggaa gacagggcac 1178

ttgggatgctc gtttttcttc taatatgttt tgagctcaag gtgatggaa atctgaaagg 1238

agtgtgctca tgccatttcc agaccaagaa aacacattta ttatttgcta attatcatag 1298

ttttgttcaa ttgcgttggt ggtttttgct atatatacac atgttgactg tca 1351

<210> 6
<211> 340
<212> PRT
<213> Homo sapiens

<220>
<223> human breast cancer amplified G-protein coupled
receptor 3-A (BCA-GPCR-3-A)

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Pro Gln His Thr Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val
20 25 30
Phe Val Leu Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu
35 40 45
Phe Ile Val Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly
50 55 60
Ile Ile Ile Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met
65 70 75 80
Tyr Phe Phe Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr
85 90 95
Ser Ile Val Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr
100 105 110
Ile Ser Tyr Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu
115 120 125
Gly Ala Thr Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr
130 135 140
Ala Ala Ile Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln
145 150 155 160
Leu Cys Leu Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr
165 170 175

Ser Met Val Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn
 180 185 190
 Asn Cys Ile Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu
 195 200 205
 Ala Cys Val Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser
 210 215 220
 Phe Val Phe Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly
 225 230 235 240
 His Ile Ala Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg
 245 250 255
 Lys Ala Phe Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe
 260 265 270
 Tyr Gly Ser Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser
 275 280 285
 His Glu Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro
 290 295 300
 Ala Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser
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 Ala Leu Arg His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys
 325 330 335
 Leu Ala Gln Ile
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<210> 7

<211> 1065

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (26)..(1030)

<223> human breast cancer amplified G-protein coupled
receptor 4 (BCA-GPCR-4)

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 1 5

agc ctt ggg gaa cac act tta cat atg ggg atg gtg aga cat acc aat 100
 Ser Leu Gly Glu His Thr Leu His Met Gly Met Val Arg His Thr Asn
 10 15 20 25

gag agc aac cta gca ggt ttc atc ctt tta ggg ttt tct gat tat gct 148
 Glu Ser Asn Leu Ala Gly Phe Ile Leu Leu Gly Phe Ser Asp Tyr Ala
 30 35 40

cag tta cag aag gtt cta ttt gtg ctc ata ttg att ctg tat tta cta 196
 Gln Leu Gln Lys Val Leu Phe Val Leu Ile Leu Ile Leu Tyr Leu Leu
 45 50 55

act att ttg ggg aat acc acc atc att ctg gtt tct cgt ctg gaa ccc 244
 Thr Ile Leu Gly Asn Thr Thr Ile Ile Leu Val Ser Arg Leu Glu Pro
 60 65 70

aag ctt cat atg ccg atg tat ttc ttc ctt tct cat ctc tcc ttc ctg 292
 Lys Leu His Met Pro Met Tyr Phe Phe Leu Ser His Leu Ser Phe Leu
 75 80 85

tac cgc tgc ttc acc agc agt gtt att ccc cag ctc ctg gta aac ctg	340
Tyr Arg Cys Phe Thr Ser Ser Val Ile Pro Gln Leu Leu Val Asn Leu	
90 95 100 105	
tgg gaa ccc atg aaa act atc gcc tat ggt ggc tgt ttg gtt cac ctt	388
Trp Glu Pro Met Lys Thr Ile Ala Tyr Gly Gly Cys Leu Val His Leu	
110 115 120	
tac aac tcc cat gcc ctg gga tcc act gag tgc gtc ctc ccg gct ctg	436
Tyr Asn Ser His Ala Leu Gly Ser Thr Glu Cys Val Leu Pro Ala Leu	
125 130 135	
atg tcc tgt gac cgc tat gtg gct gtc tgc cgt cct ctc cat tac act	484
Met Ser Cys Asp Arg Tyr Val Ala Val Cys Arg Pro Leu His Tyr Thr	
140 145 150	
gtc tta atg cat atc cat ctc tgc atg gcc ttg gca tct atg gca tgg	532
Val Leu Met His Ile His Leu Cys Met Ala Leu Ala Ser Met Ala Trp	
155 160 165	
ctc agt gga ata gcc acc acc ctg gta cag tcc acc ctc acc ctg cag	580
Leu Ser Gly Ile Ala Thr Thr Leu Val Gln Ser Thr Leu Thr Leu Gln	
170 175 180 185	
ctg ccc ttc tgt ggg cat cgc caa gtg gat cat ttc atc tgc gag gtc	628
Leu Pro Phe Cys Gly His Arg Gln Val Asp His Phe Ile Cys Glu Val	
190 195 200	
cct gtg ctc atc aag ctg gct tgt gtg ggc acc acg ttt aac gag gct	676
Pro Val Leu Ile Lys Leu Ala Cys Val Gly Thr Thr Phe Asn Glu Ala	
205 210 215	
gag ctt ttt gtg gct agt atc ctt ttc ctt ata gtg cct gtc tca ttc	724
Glu Leu Phe Val Ala Ser Ile Leu Phe Leu Ile Val Pro Val Ser Phe	
220 225 230	
atc ctg gtc tcc tct ggc tac att gcc cac gca gtg ttg agg att aag	772
Ile Leu Val Ser Ser Gly Tyr Ile Ala His Ala Val Leu Arg Ile Lys	
235 240 245	
tca gct acc ggg aga cag aaa gca ttc ggg acc tgc ttc tcc cac ctg	820
Ser Ala Thr Gly Arg Gln Lys Ala Phe Gly Thr Cys Phe Ser His Leu	
250 255 260 265	
aca gtg gtc acc atc ttt tat gga acc atc atc ttc atg tat ctg cag	868
Thr Val Val Thr Ile Phe Tyr Gly Thr Ile Ile Phe Met Tyr Leu Gln	
270 275 280	
cca gcc aag agt aga tcc agg gac cag ggc aag ttt gtt tct ctc ttc	916
Pro Ala Lys Ser Arg Ser Arg Asp Gln Gly Lys Phe Val Ser Leu Phe	
285 290 295	
tac act gtg gta acc cgc atg ctt aac cct ctt att tat acc ttg agg	964
Tyr Thr Val Val Thr Arg Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg	
300 305 310	
atc aag gag gtg aaa ggg gca tta aag aaa gtt cta gca aag gct ctg	1012
Ile Lys Glu Val Lys Gly Ala Leu Lys Lys Val Leu Ala Lys Ala Leu	
315 320 325	

gga gta aat att tta tga ttattaaaaa aaaatttaag tgacactgtg atgaa 1065
 Gly Val Asn Ile Leu
 330 335

<210> 8
 <211> 334
 <212> PRT
 <213> Homo sapiens

<220>
 <223> human breast cancer amplified G-protein coupled
 receptor 4 (BCA-GPCR-4)

<400> 8
 Met Cys Tyr Leu Ser Gln Leu Cys Leu Ser Leu Gly Glu His Thr Leu
 1 5 10 15
 His Met Gly Met Val Arg His Thr Asn Glu Ser Asn Leu Ala Gly Phe
 20 25 30
 Ile Leu Leu Gly Phe Ser Asp Tyr Ala Gln Leu Gln Lys Val Leu Phe
 35 40 45
 Val Leu Ile Leu Ile Leu Tyr Leu Leu Thr Ile Leu Gly Asn Thr Thr
 50 55 60
 Ile Ile Leu Val Ser Arg Leu Glu Pro Lys Leu His Met Pro Met Tyr
 65 70 75 80
 Phe Phe Leu Ser His Leu Ser Phe Leu Tyr Arg Cys Phe Thr Ser Ser
 85 90 95
 Val Ile Pro Gln Leu Leu Val Asn Leu Trp Glu Pro Met Lys Thr Ile
 100 105 110
 Ala Tyr Gly Gly Cys Leu Val His Leu Tyr Asn Ser His Ala Leu Gly
 115 120 125
 Ser Thr Glu Cys Val Leu Pro Ala Leu Met Ser Cys Asp Arg Tyr Val
 130 135 140
 Ala Val Cys Arg Pro Leu His Tyr Thr Val Leu Met His Ile His Leu
 145 150 155 160
 Cys Met Ala Leu Ala Ser Met Ala Trp Leu Ser Gly Ile Ala Thr Thr
 165 170 175
 Leu Val Gln Ser Thr Leu Thr Leu Gln Leu Pro Phe Cys Gly His Arg
 180 185 190
 Gln Val Asp His Phe Ile Cys Glu Val Pro Val Leu Ile Lys Leu Ala
 195 200 205
 Cys Val Gly Thr Thr Phe Asn Glu Ala Glu Leu Phe Val Ala Ser Ile
 210 215 220
 Leu Phe Leu Ile Val Pro Val Ser Phe Ile Leu Val Ser Ser Gly Tyr
 225 230 235 240
 Ile Ala His Ala Val Leu Arg Ile Lys Ser Ala Thr Gly Arg Gln Lys
 245 250 255
 Ala Phe Gly Thr Cys Phe Ser His Leu Thr Val Val Thr Ile Phe Tyr
 260 265 270
 Gly Thr Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Arg Ser Arg
 275 280 285
 Asp Gln Gly Lys Phe Val Ser Leu Phe Tyr Thr Val Val Thr Arg Met
 290 295 300
 Leu Asn Pro Leu Ile Tyr Thr Leu Arg Ile Lys Glu Val Lys Gly Ala
 305 310 315 320
 Leu Lys Lys Val Leu Ala Lys Ala Leu Gly Val Asn Ile Leu
 325 330

<210> 9
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-1

 <400> 9
 atgttgggga acgtcgccat c 21

 <210> 10
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-1

 <400> 10
 tcattccacag agcctccaga t 21

 <210> 11
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-2

 <400> 11
 atgggaaagg acaatccagt t 21

 <210> 12
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-2

 <400> 12
 ctaagagagt aactccagca a 21

 <210> 13
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-3

<400> 13
 atggaaatag ccaatgtgag ttc 23

<210> 14
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-3

<400> 14
 taaatttgcg ccagcttgcc tg 22

<210> 15
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-4

<400> 15
 atggtgagac ataccaatga gag 23

<210> 16
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR
 amplification primer for BCA-GPCR-4

<400> 16
 cataaaatat ttactccag agcc 24

<210> 17
 <211> 1011
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1011)
 <223> human breast cancer amplified G-protein coupled
 receptor 3-B (BCA-GPCR-3-B)

<400> 17
 atg ccc tgt gct ctt ccc aca ggt ggc ctt ttg ccc cac ccc cag cat 48
 Met Pro Cys Ala Leu Pro Thr Gly Gly Leu Leu Pro His Pro Gln His
 1 5 10 15

aca atg atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc	96
Thr Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu	
20 25 30	
ctg ggc ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt	144
Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val	
35 40 45	
gtc ttg agt ttt tac atg gta tgc atc ttg ggc aat ggc atc atc att	192
Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile	
50 55 60	
ctg gtc tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt	240
Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe	
65 70 75 80	
ctt gcc aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc	288
Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val	
85 90 95	
cca cag ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat	336
Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr	
100 105 110	
gga ggg tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc	384
Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr	
115 120 125	
gag tgt gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc	432
Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile	
130 135 140	
tgc agg cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt	480
Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu	
145 150 155 160	
ggg cta gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg	528
Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val	
165 170 175	
ggc tcc acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc	576
Gly Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile	
180 185 190	
gac cac ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg	624
Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val	
195 200 205	
gat acc agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt	672
Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe	
210 215 220	
gtt gtc ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc	720
Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala	
225 230 235 240	
cgg gcc gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc	768
Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe	
245 250 255	

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aac acc tgt tct tcc cac gtg gct gtg gtg tct ctg ttt tac ggg agc      816
Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser
      260                                265

atc atc ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag      864
Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln
      275                                280                                285

ggc aag ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac      912
Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn
      290                                295                                300

cca ctt att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg      960
Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg
      305                                310                                315                                320

cac atg gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa      1008
His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
      325                                330                                335

att
Ile

1011

<210> 18
<211> 337
<212> PRT
<213> Homo sapiens

<220>
<223> human breast cancer amplified G-protein coupled
      receptor 3-B (BCA-GPCR-3-B)

<400> 18
Met Pro Cys Ala Leu Pro Thr Gly Gly Leu Leu Pro His Pro Gln His
      1      5      10      15
Thr Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu
      20      25      30
Leu Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val
      35      40      45
Val Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile
      50      55      60
Leu Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe
      65      70      75      80
Leu Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val
      85      90      95
Pro Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr
      100      105      110
Gly Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr
      115      120      125
Glu Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile
      130      135      140
Cys Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu
      145      150      155      160
Gly Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val
      165      170      175
Gly Ser Thr Leu Thr Met Leu Leu Pro Cys Gly Asn Asn Cys Ile
      180      185      190
Asp His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val
      195      200      205

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Asp Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe
  210          215          220
Val Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala
  225          230          235          240
Arg Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe
          245          250          255
Asn Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser
  260          265          270
Ile Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln
  275          280          285
Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn
  290          295          300
Pro Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg
  305          310          315          320
His Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln
          325          330          335
Ile

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<210> 19
<211> 960
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(960)
<223> human breast cancer amplified G-protein coupled
      receptor 3-C (BCA-GPCR-3-C)

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<400> 19
atg atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc ctg 48
Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
  1          5          10          15

ggc ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt gtc 96
Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
          20          25          30

ttg agt ttt tac atg gta tcg atc ttg ggc aat ggc atc atc att ctg 144
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu
          35          40          45

gtc tcc cat aca gat gtg cac ctc cac aca cct atg tac ttc ttt ctt 192
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
          50          55          60

gcc aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc cca 240
Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
          65          70          75          80

cag ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat gga 288
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
          85          90          95

ggg tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc gag 336
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
          100          105          110

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tgt gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc tgc	384
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys	
115 120 125	
agg cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt ggg	432
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly	
130 135 140	
cta gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg ggc	480
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Ser Met Val Gly	
145 150 155 160	
tcc acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc gac	528
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp	
165 170 175	
cac ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg gat	576
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp	
180 185 190	
acc agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt gtt	624
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val	
195 200 205	
gtc ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc cgg	672
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg	
210 215 220	
gcc gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc aac	720
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn	
225 230 235 240	
acc tgt tct tcc cac gtg gct gtg gtg tct ctg ttt tac ggg agc atc	768
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile	
245 250 255	
atc ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag ggc	816
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly	
260 265 270	
aag ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac cca	864
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro	
275 280 285	
ctt att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg cac	912
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His	
290 295 300	
atg gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa att	960
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile	
305 310 315 320	

<210> 20

<211> 320

<212> PRT

<213> Homo sapiens

<220>

<223> human breast cancer amplified G-protein coupled
receptor 3-C (BCA-GPCR-3-C)

```

<400> 20
Met Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu
 1          5          10          15
Gly Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val
 20          25          30
Leu Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Leu
 35          40          45
Val Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu
 50          55          60
Ala Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro
 65          70          75          80
Gln Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly
 85          90          95
Gly Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu
100          105          110
Cys Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys
115          120          125
Arg Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly
130          135          140
Leu Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly
145          150          155          160
Ser Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp
165          170          175
His Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp
180          185          190
Thr Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val
195          200          205
Val Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg
210          215          220
Ala Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn
225          230          235          240
Thr Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile
245          250          255
Ile Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly
260          265          270
Lys Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro
275          280          285
Leu Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His
290          295          300
Met Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
305          310          315          320

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<210> 21

<211> 957

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(957)

<223> human breast cancer amplified G-protein coupled
receptor 3-D (BCA-GPCR-3-D)

<400> 21

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atg gaa ata gcc aat gtg agt tct cca gaa gtc ttt gtc ctc ctg ggc 48
Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly
 1          5          10          15

```

ttc tcc gca cga ccc tca cta gaa act gtc ctc ttc ata gtt gtc ttg	96
Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu	
20 25 30	
agt ttt tac atg gta tcg atc ttg ggc aat ggc atc atc att ctg gtc	144
Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val	
35 40 45	
tcc cat aca gat gtg cac ctc ctc aca cct atg tac ttc ttt ctt gcc	192
Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala	
50 55 60	
aac ctc tcc ttc ctg gac atg agc ttc acc acg agc att gtc cca cag	240
Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln	
65 70 75 80	
ctc ctg gct aac ctc tgg gga cca cag aaa acc ata agc tat gga ggg	288
Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly	
85 90 95	
tgt gtg gtc cag ttc tat atc tcc cat tgg ctg ggg gca acc gag tgt	336
Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys	
100 105 110	
gtc ctg ctg gcc acc atg tcc tat gac cgc tac gct gcc atc tgc agg	384
Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg	
115 120 125	
cca ctc cat tac act gtc att atg cat cca cag ctt tgc ctt ggg cta	432
Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu	
130 135 140	
gct ttg gcc tcc tgg ctg ggg ggt ctg acc acc agc atg gtg ggc tcc	480
Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser	
145 150 155 160	
acg ctc acc atg ctc cta ccg ctg tgt ggg aac aat tgc atc gac cac	528
Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His	
165 170 175	
ttc ttt tgc gag atg ccc ctc att atg caa ctg gct tgt gtg gat acc	576
Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr	
180 185 190	
agc ctc aat gag atg gag atg tac ctg gcc agc ttt gtc ttt gtt gtc	624
Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val	
195 200 205	
ctg cct ctg ggg ctc atc ctg gtc tct tac ggc cac att gcc cgg gcc	672
Leu Pro Leu Gly Phe Leu Val Ser Tyr Gly His Ile Ala Arg Ala	
210 215 220	
gtg ttg aag atc agg tca gca gaa ggg cgg aga aag gca ttc aac acc	720
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr	
225 230 235 240	
tgt tct tcc cac gtg gct gtg gtg tct ctg ttt tac ggg agc atc atc	768
Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile	
245 250 255	

ttc atg tat ctc cag cca gcc aag agc acc tcc cat gag cag ggc aag 816
Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys
260 265 270

ttc ata gct ctg ttc tac acc gta gtc act cct gcg ttg aac cca ctt 864
Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
275 280 285

att tac acc ctg agg aac acg gag gtg aag agc gcc ctc cgg cac atg 912
Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met
290 295 300

gta tta gag aac tgc tgt ggc tct gca ggc aag ctg gcg caa att 957
Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
305 310 315

<210> 22

<211> 319

<212> PRT

<213> Homo sapiens

<220>

<223> human breast cancer amplified G-protein coupled
receptor 3-D (BCA-GPCR-3-D)

<400> 22

Met Glu Ile Ala Asn Val Ser Ser Pro Glu Val Phe Val Leu Leu Gly
1 5 10 15
Phe Ser Ala Arg Pro Ser Leu Glu Thr Val Leu Phe Ile Val Val Leu
20 25 30
Ser Phe Tyr Met Val Ser Ile Leu Gly Asn Gly Ile Ile Ile Leu Val
35 40 45
Ser His Thr Asp Val His Leu His Thr Pro Met Tyr Phe Phe Leu Ala
50 55 60
Asn Leu Ser Phe Leu Asp Met Ser Phe Thr Thr Ser Ile Val Pro Gln
65 70 75 80
Leu Leu Ala Asn Leu Trp Gly Pro Gln Lys Thr Ile Ser Tyr Gly Gly
85 90 95
Cys Val Val Gln Phe Tyr Ile Ser His Trp Leu Gly Ala Thr Glu Cys
100 105 110
Val Leu Leu Ala Thr Met Ser Tyr Asp Arg Tyr Ala Ala Ile Cys Arg
115 120 125
Pro Leu His Tyr Thr Val Ile Met His Pro Gln Leu Cys Leu Gly Leu
130 135 140
Ala Leu Ala Ser Trp Leu Gly Gly Leu Thr Thr Ser Met Val Gly Ser
145 150 155 160
Thr Leu Thr Met Leu Leu Pro Leu Cys Gly Asn Asn Cys Ile Asp His
165 170 175
Phe Phe Cys Glu Met Pro Leu Ile Met Gln Leu Ala Cys Val Asp Thr
180 185 190
Ser Leu Asn Glu Met Glu Met Tyr Leu Ala Ser Phe Val Phe Val Val
195 200 205
Leu Pro Leu Gly Leu Ile Leu Val Ser Tyr Gly His Ile Ala Arg Ala
210 215 220
Val Leu Lys Ile Arg Ser Ala Glu Gly Arg Arg Lys Ala Phe Asn Thr
225 230 235 240
Cys Ser Ser His Val Ala Val Val Ser Leu Phe Tyr Gly Ser Ile Ile
245 250 255
Phe Met Tyr Leu Gln Pro Ala Lys Ser Thr Ser His Glu Gln Gly Lys
260 265 270

Phe Ile Ala Leu Phe Tyr Thr Val Val Thr Pro Ala Leu Asn Pro Leu
 275 280 285
 Ile Tyr Thr Leu Arg Asn Thr Glu Val Lys Ser Ala Leu Arg His Met
 290 295 300
 Val Leu Glu Asn Cys Cys Gly Ser Ala Gly Lys Leu Ala Gln Ile
 305 310 315

<210> 23
 <211> 1020
 <212> DNA
 <213> Homo sapiens

<220>
 <223> human breast cancer amplified G-protein coupled
 receptor 3-A (BCA-GPCR-3-A) cDNA

<220>
 <221> CDS
 <222> (1)..(1020)
 <223> human breast cancer amplified G-protein coupled
 receptor 3-A (BCA-GPCR-3-A)

<400> 23
 atgacctgta tgcacctgtgc tcttcccaca ggtggccttt tgccccccccc ccagcatata 60
 atgatggaaa tagccaatgt gagttctcca gaagtctttg tctctcctggg cttctccgga 120
 cgacctcac tagaaactgt cctcttcata gttgtcttga gtttttaccat ggtatcgatc 180
 ttgggcaatg gcatcatcat tctggctctc catcacagatg tgcacctcca cacacctatg 240
 tactttcttc ttgccaacct ctctctctctg gacatgagct tcaccacgag cattgtccca 300
 cagctctctg ctaacctctg gggaccacag aaaaccataa gctatggagg gtgtgtgggtc 360
 cagttctata tctcccattg gctgggggca accgagtggt tctgtctggc caccatgtcc 420
 tatgaccgct acgctgccat ctgcaggcca ctccattaca ctgtcattat gcattccacag 480
 ctttgctctg ggctagcttt ggctctctgg ctgggggggtc tgaccaccag catgggtgggc 540
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